

1645

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P#9

RAW SEQUENCE LISTING

DATE: 09/04/2002

PATENT APPLICATION: US/09/724,586

TIME: 11:57:34

Input Set : N:\Crf3\RULE60\09724586.raw

Output Set: N:\CRF4\09042002\I724586.raw

1 <110> APPLICANT: Sakowicz, Roman  
 2 Goldstein, Lawrence S. B.  
 3 The Regents of the University of California  
 4 <120> TITLE OF INVENTION: Identification and Expression of a Novel Kinesin Motor  
 5 Protein  
 6 <130> FILE REFERENCE: 18557C-000710US  
 7 <140> CURRENT APPLICATION NUMBER: 09/724,586  
 8 <141> CURRENT FILING DATE: 2000-11-28  
 10 <150> PRIOR APPLICATION NUMBER: US/09/235,416  
 11 <151> PRIOR FILING DATE: 1999-01-22  
 14 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/01355  
 15 <151> PRIOR FILING DATE: 1999-01-22  
 16 <150> PRIOR APPLICATION NUMBER: US 60/072,361  
 17 <151> PRIOR FILING DATE: 1998-01-23  
 18 <160> NUMBER OF SEQ ID NOS: 7  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 784  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Thermomyces lanuginosus  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed  
 27 microtubule motor protein  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: DOMAIN  
 30 <222> LOCATION: (1)..(357)  
 31 <223> OTHER INFORMATION: kinesin-like microtubule motor domain  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: DOMAIN  
 34 <222> LOCATION: (358)..(442)  
 35 <223> OTHER INFORMATION: neck domain links motor domain to stalk domain  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: DOMAIN  
 38 <222> LOCATION: (443)..(601)  
 39 <223> OTHER INFORMATION: stalk domain, unc-104 family domain  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: DOMAIN  
 42 <222> LOCATION: (602)..(784)  
 43 <223> OTHER INFORMATION: tail domain  
 44 <400> SEQUENCE: 1  
 45 Met Ser Gly Gly Gly Asn Ile Lys Val Val Val Arg Val Arg Pro Phe  
 46 1 5 10 15  
 47 Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu

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48		20		25		30	
49	Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala						
50		35		40		45	
51	Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe						
52		50		55		60	
53	Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg						
54		65		70		75	
55	Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala						
56			85		90		95
57	Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser						
58		100		105		110	
59	Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile						
60		115		120		125	
61	Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys						
62		130		135		140	
63	Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr						
64		145		150		155	160
65	Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu						
66			165		170		175
67	Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala						
68		180		185		190	
69	Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu						
70		195		200		205	
71	Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser						
72		210		215		220	
73	Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His						
74		225		230		235	240
75	Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu						
76			245		250		255
77	Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly						
78		260		265		270	
79	Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu						
80		275		280		285	
81	Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys						
82		290		295		300	
83	Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu						
84		305		310		315	320
85	Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile						
86			325		330		335
87	Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr						
88		340		345		350	
89	Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp						
90		355		360		365	
91	Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu						
92		370		375		380	
93	Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly						
94		385		390		395	400
95	Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu						
96			405		410		415

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```

97      Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
98              420              425              430
99      Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
100             435              440              445
101      Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
102             450              455              460
103      Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Gly Ile Ser Ile
104             465              470              475              480
105      Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
106              485              490              495
107      Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
108              500              505              510
109      Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
110              515              520              525
111      Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
112              530              535              540
113      Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
114             545              550              555              560
115      Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
116              565              570              575
117      Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
118              580              585              590
119      His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
120              595              600              605
121      His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
122              610              615              620
123      Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
124             625              630              635              640
125      Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
126              645              650              655
127      Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
128              660              665              670
129      Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
130              675              680              685
131      Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
132             690              695              700
133      Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
134             705              710              715              720
135      Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
136              725              730              735
137      Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
138              740              745              750
139      Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
140             755              760              765
141      Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
142             770              775              780
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 2352
146 <212> TYPE: DNA

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```

147 <213> ORGANISM: Thermomyces lanuginosus
148 <220> FEATURE:
149 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
150 microtubule motor protein
151 <400> SEQUENCE: 2
152 atgtcgggcg gtggaaatat caaggtggtg gtgcgggtac gcccgttcaa cgcccagaaa 60
153 atcgaccgtg gcgcaaaatg tattgtgcgg atggaaggaa atcaaaccat cctcaccctt 120
154 cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
155 gcatttgctg tgcgtcggtc gtattggtcc ttgacaaga atgctcccaa ctatgegaga 240
156 caggaagacc tattccaaga tctcgagtc ccgcttctgg ataatgcatt caagggttat 300
157 aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
158 tatggcaagg agcatggcgt gatcccgcg atttgccagg acatgttccg gcgtattaat 420
159 gaactgcaga aggacaagaa cctcacttgc accgtcgaag tttcgtactt ggaaatttac 480
160 aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
161 caccgcgcga ccggccccta cgtggaggac ttggcgaagc tggctcgtgc atcattccaa 600
162 gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaacatg 660
163 aacgagacat ccagtcgatc ccacgcgcgc ttcactttga ccttgacgca aaagtggcat 720
164 gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
165 ggttctgagc gagcaacgct caccggagct actggagcgc gactgaagga ggggtgcagag 840
166 atcaaccgct cactttcgac cctaggctgt gtgattgcag cgctagcgga tatgtcgtcg 900
167 ggaaaacaga agaagaatca gttagtacct taccgagatt cgggtactgac gtggcttctg 960
168 aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat 1020
169 attaatcttg aagagactct cagtaccctt cgaatagcgg actctgcgaa gcgaatcaag 1080
170 aaccacgcag tggatcaatga agaccggaac gcgcggatga tccgcgagtt gaaggaggaa 1140
171 ctgcgcgagc tgaggagcaa actccagagc agtgggtggag gtggagggtg tgaggagggt 1200
172 tctggcgggc cagtggagga atcgtaaccg ccgacacgc cgctcgagaa gcaaatcgtg 1260
173 tcgattcagc agccggatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa 1320
174 ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
175 aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
176 gaaaagggct ttgttggtcc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
177 gatgactctc ttctggctga gtgtcttgtc tacaacatca agcccgggca gacaagggtt 1560
178 ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
179 gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
180 gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgcag cggctacagg 1740
181 atcatcctgg gcgatttcca catttttoga ttcaaccatc cggaagaagc tcgtgcggaa 1800
182 cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttgcctgctc 1860
183 ccaggccgct acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
184 tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg 1980
185 gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag 2040
186 ttgatgcat tatttgacga tgttcagaaa gcgcgggcag ttctgctggt gctggtcgaa 2100
187 gacaacgaag atagcgattc gcagagttcg tttccggtcc gtgacaaata catgtccaat 2160
188 ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt 2220
189 gatgacgagc gtgacgcgct gttttttggt gataagaagt cgaaacagga tgcgtctaata 2280
190 gttgatgttg aggagttgcy tcaacagcag gctcagatgg aagaagccct gaaaacagcg 2340
191 aagcaggaat tc 2352
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 21
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence

```

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```

197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
199 <400> SEQUENCE: 3
200     atgtcgggcg gtggaaatat c                               21
202 <210> SEQ ID NO: 4
203 <211> LENGTH: 23
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
208 <400> SEQUENCE: 4
209     gaattcctgc ttcgctgttt tca                               23
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 30
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
217     forward primer
218 <220> FEATURE:
219 <221> NAME/KEY: modified_base
220 <222> LOCATION: (25)
221 <223> OTHER INFORMATION: n = a, c, g or t
222 <400> SEQUENCE: 5
W--> 223     gcgcggatcc atytttygcht ayggncarac                     30
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 30
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
231     reverse primer
232 <220> FEATURE:
233 <221> NAME/KEY: modified_base
234 <222> LOCATION: (16)
235 <223> OTHER INFORMATION: n = a, c, g or t
236 <220> FEATURE:
237 <221> NAME/KEY: modified_base
238 <222> LOCATION: (28)
239 <223> OTHER INFORMATION: n = a, c, g or t
240 <400> SEQUENCE: 6
W--> 241     gcgcgaattc tcdganccdg cvarrtcnac                     30
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 30
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
249     reverse primer

```

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/04/2002  
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Input Set : N:\Crf3\RULE60\09724586.raw  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 25  
Seq#:6; N Pos. 16,28  
Seq#:7; N Pos. 16,28

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09724586.raw

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L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0